

# Package ‘GeneF’

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**Type** Package

**Title** Package for Generalized F-statistics

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**Description** This package implements several generalized F-statistics.  
The current version includes a generalized F-statistic based on  
the flexible isotonic/monotonic regression or order restricted hypothesis testing.

**License** GPL (>= 2)

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## Description

These functions test the hypothesis regarding population means from ordered sample groups. Restrictions like a weakly/general/strongly isotonic/monotonic order as well as a lower bound for the location can be imposed on the population means. A partition of sample groups and the corresponding estimates of population means are also provided.

## Usage

```
flexisoreg(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexisoreg.stat(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexmonoreg(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
flexmonoreg.stat(y, x, lambda = 0, alpha.location = 1, alpha.adjacency = 0.5)
```

## Arguments

y	a vector of observed data
x	a vector of ordinal group labels corresponding to y but not necessarily sorted
lambda	a lower location bound for partitioned groups other than the first one
alpha.location	$\alpha$ level for the upper-tailed one-sample <i>t</i> -test with lower bound lambda
alpha.adjacency	$\alpha$ level for the upper-tailed two-sample <i>t</i> -test to evaluate the magnitude of non-decreasing order

## Details

flexisoreg is used for flexible nondecreasing order restricted hypothesis testing. flexmonoreg is used for flexible nondecreasing or nonincreasing order restricted hypothesis testing. flexisoreg.stat and flexmonoreg.stat only return an *F*-statistic, which is convenient for multiple comparison.

## Value

groups	A partition of sample groups
estimates	estimated population means
statistic	an <i>F</i> -type statistic from the test

## Note

Since the *p*-value of test has to be evaluated by permutation method, these functions will not return any *p*-value. For the permutation *p*-value of an individual test, see flexisoreg.pvalue and flexmonoreg.pvalue. For the pooled permutation *p*-values of multiple tests, see flexisoreg.poolpvalues and flexmonoreg.poolpvalues.

**Author(s)**

Yinglei Lai ylai@gwu.edu

**References**

Yinglei Lai (2007) A flexible order restricted hypothesis testing and its application to gene expression data. Technical Report

**Examples**

```
#generate ordinal group labels x
x <- runif(100)*6
x <- round(x,0)/3
#generate true values z
z <- round(x^2,0)
#generate observed values y
y <- z + rnorm(100)

#print default results
print(rbind(x,z,y))
print(flexisoreg(y,x))
print(flexisoreg.stat(y,x))
print(flexisoreg(y,0-x))
print(flexisoreg.stat(y,0-x))
print(flexmonoreg(y,x))
print(flexmonoreg.stat(y,x))

#plots for illustration
par(mfrow=c(2,3), mai=c(0.6, 0.6, 0.3, 0.1))
plot(x,y, main="True Model",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, z, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=1, alpha.location=0.05, alpha.adjacency=1)
plot(x,y, main="Location Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=1, alpha.location=0.05, alpha.adjacency=0.05)
plot(x,y, main="Location and Strong Order Restrictions",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.95)
plot(x,y, main="Weak Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5)
plot(x,y, main="General Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)

results <- flexisoreg(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.05)
plot(x,y, main="Strong Order Restriction",cex.axis=1.5, cex.lab=1.5, cex.main=1.5, cex=1.5)
```

```
lines(x, results$estimate, type="p", pch=15, col="black", cex=2.5)
```

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flexorhtest.pvalue	<i>Significance Assessment for the Flexible Order Restricted Hypothesis Testing</i>
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### Description

These functions evaluate the  $p$ -values from an individual or multiple flexible order restricted hypothesis testing.

### Usage

```
flexisoreg.pvalue(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexisoreg.poolpvalues(m, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexmonoreg.pvalue(y, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
flexmonoreg.poolpvalues(m, x, lambda=0, alpha.location=1, alpha.adjacency=0.5, B=100)
```

### Arguments

<code>m</code>	a matrix of observed data, where samples are in columns and variables are in rows
<code>y</code>	a vector of observed data
<code>x</code>	a vector of ordinal group labels corresponding to <code>y</code> or rows of <code>m</code> but not necessarily sorted
<code>lambda</code>	a lower location bound for partitioned groups other than the first one
<code>alpha.location</code>	$\alpha$ level for the upper-tailed one-sample $t$ -test with lower bound <code>lambda</code>
<code>alpha.adjacency</code>	$\alpha$ level for the upper-tailed two-sample $t$ -test to evaluate the magnitude of non-decreasing order
<code>B</code>	the number of permutations for $p$ -value assessment

### Details

`flexisoreg.pvalue` and `flexmonoreg.pvalue` provide the permutation  $p$ -value for an individual flexible order restricted hypothesis testing. `flexisoreg.poolpvalues` and `flexmonoreg.poolpvalues` provide the pooled permutation  $p$ -values for multiple flexible order restricted hypothesis testing.

### Value

`flexisoreg.pvalue` and `flexmonoreg.pvalue` return a permutation  $p$ -value. `flexisoreg.poolpvalues` and `flexmonoreg.poolpvalues` return a vector of pooled permutation  $p$ -values.

**Note**

These functions are used in conjunction with flexisoreg, flexisoreg.stat, flexmonoreg and flexmonoreg.stat.

**Author(s)**

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**References**

Yinglei Lai (2007) A flexible order restricted hypothesis testing and its application to gene expression data. Technical Report

**Examples**

```
#generate ordinal group labels x
x <- runif(100)*6
x <- round(x,0)/3
#generate true values z
z <- round(x^2,0)
#generate 6 vectors in a matrix for observed values, some noises and some not
m <- array(double(6*100), dim=c(6,100))
for(k in 1:3)
m[k,] <- rnorm(100)
for(k in 4:6)
m[k,] <- z + rnorm(100)

#print default results
par(mfrow=c(2,3))
for(k in 1:6){
print(paste("The ", k, "-th vector", sep=""))
y <- m[k,]
plot(x,y,main=k)
print(flexisoreg.stat(y,x))
print(flexisoreg.pvalue(y,x,B=20))
print(flexisoreg.stat(y,0-x))
print(flexisoreg.pvalue(y,0-x,B=20))
print(flexmonoreg.stat(y,x))
print(flexmonoreg.pvalue(y,x,B=20))
}

flexisoreg.poolpvalues(m, x, B=20)
flexmonoreg.poolpvalues(m, x, B=20)
```

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GeneF

*Package for Generalized F-statistics*

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### Description

This package implements several generalized  $F$ -statistics. The current version includes a generalized  $F$ -statistic based on the flexible isotonic/monotonic regression or order restricted hypothesis testing.

### Details

Package: GeneF  
Type: Package  
Version: 1.0  
Date: 2007-07-18  
License: GPL version 2 or newer

### Author(s)

Yinglei Lai  
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internal functions

*Internal GeneF Functions*

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### Description

Internal functions to support generalized  $F$ -statistics.

### Usage

```
get.numbers(x)
t1p1(v, n)
t1p2(v, n1, n2)
```

### Arguments

`x` a vector of ordered groups of numbers  
`v` a vector of real numbers  
`n` the sample size of one-sample data  
`n1` the first sample size of two-sample data  
`n2` the second sample size of two-sample data

**Value**

<code>get.numbers</code>	a vector of culmulative sample sizes from ordered groups
<code>t1p1</code>	a $p$ -value from one-sample $t$ -test
<code>t1p2</code>	a $p$ -value from two-sample $t$ -test

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